Amendments to the Claims:

Please amend the claims as follows:

1. (currently amended) A method for sequence-specifc identification, separation and quantitation of polynucleotide fragments in ~~amplification of~~ a population of polynucleotides comprising:

(a) reverse transcribing an RNA population to provide a double-stranded cDNA population;

(b) digesting said cDNA population with one or more restriction endonucleases having a degenerate recognition or cleavage sequence, wherein said restriction endonuclease is a three- to eight-base cutter and wherein the degenerate recognition or cleavage sequence is represented by the formula of N^m, where N is the extent of degeneracy, and m is the number of degenerate bases, and wherein for at least one of said restriction endonucleases N is 2-4 and m is 1-5, to produce restriction fragments having N^m different single-stranded overhangs for each restriction endonuclease;

(c) ligating said restriction fragments to a series of adapters lacking restriction endonuclease sites, each adapter having a sequence complementary to one of said overhangs such that restriction fragments having identical overhangs are ligated to the same adapter; [[and]]

(d) amplifying said restriction fragments for no more than 25 cycles with a primer comprising a detectable label; and

(e) detecting and quantifying said polynucleotide fragments.

2. (original) The method of claim 1 wherein for at least one of said restriction endonucleases m is 2, 3 or 4.

3. (original) The method of claim 1 wherein said restriction endonuclease comprises a four-base cutter.

4. (original) The method of claim 1 further comprising digesting the restriction fragments obtained in (b) with one or more further restriction endonucleases producing restriction fragments with single-stranded overhangs different from those produced in (b).

5. (original) The method of claim 4 further comprising ligating the single-stranded overhangs produced by the digesting of claim 4 to a series of adapters each adaptor having a sequences complementary to one of said overhangs.

6. (original) The method of claim 1 wherein said restriction fragments of (d) are amplified by the polymerase chain reaction (PCR) to produce PCR products.

7. (original) The method of claim 6 wherein said adapters provide priming sites for said polymerase chain reaction.

8. (original) The method of claim 6 further comprising detecting the PCR products.

9-23. (cancelled)